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ClustalW Results

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SEQIDNO:6
gi13448825|JAM3

CLUSTAL W (1.7) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQIDNO_6 310 aa

Sequence 2: gi13448825|JAM3 310 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 99

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:4221

Alignment Score 1954

CLUSTAL-Alignment file created [baaiPaWsX.aln]

CLUSTAL W (1.7) multiple sequence alignment

```
SEQIDNO_6      MALRRPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT
gi13448825|JAM3 MALRRPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT
*****
```

```
SEQIDNO_6      SDPRI EWKKIQDEQTTYVFFDNKI QGDLAGRAEILGKTS LKIWNVTRRDSALYRCEVVAR
gi13448825|JAM3 SDPRI EWKKIQDEQTTYVFFDNKI QGDLAGRAEILGKTS LKIWNVTRRDSALYRCEVVAR
*****
```

```
SEQIDNO_6      NDRKEIDEIVIELTVQVKPVT P VCRVPKAVPVGKMATLHCQES EGHPRPHYSWYRNDVPL
gi13448825|JAM3 NDRKEIDEIVIELTVQVKPVT P VCRVPKAVPVGKMATLHCQES EGHPRPHYSWYRNDVPL
*****
```

```
SEQIDNO_6      PTDSRANPRFRNSSSHL NSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDL
gi13448825|JAM3 PTDSRANPRFRNSSSHL NSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDL
*****
```

SEQIDNO_6
gi13448825|JAM3
NIGGIIGGVLVVLAVLALITLGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG
NIGGIIGGVLVVLAVLALITLGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG

SEQIDNO_6
gi13448825|JAM3
DFRHKSSFVI
DFRHKSSFVI

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Cluster Results

Sequences Help

Retrieval	BLAST2	FASTA	ClustalW	GGC Assembly	Phrap	Translation
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SEQIDNO:25
gi13448824|JAM3

CLUSTAL W (1.7) Multiple Sequence Alignments

```
Sequence format is Pearson           1956 bp
Sequence 1: SEQIDNO_25
Sequence 2: g114446824/JM3          933 bp
Start of pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 99
There are Multiple Alignment
There are 1 groups
Aligning...
Group 1: Sequences: 2      Score:17708
Alignment Score 6651
CUSTAL-Alignment file created [baser7a4ex.aln]
CUSTAL W (1.7) multiple sequence alignment
```

[illegible]

SBQIND_25
g113448824 |JMB3

CAAGATCGATGAGGAAAAATTCCAGAGAGAGCAAAACACACATATGTGTGTTTTCAGACAAA
CAGATTCGATGTGAGAGAAATTTCAGAGAGAGAAACACACATATGTGTGTTTTCAGACAAA

AAATTCAGAGGAGATTTGAGCGGGGTGTGTGACAGAAATACATGGGAGAGACATCCGTGAGATATG
AAATTCAGAGGAGATTTGAGCGGGGTGTGTGACAGAAATACATGGGAGAGACATCCGTGAGATATG

GAATGTGACACAGAGAGAGCTCAGACCTTTTATACGTGTGAGAGAGGTGTGTGTCAGAAATGACCCG
GAATGTGACACAGAGAGAGCTCAGACCTTTTATACGTGTGAGAGAGGTGTGTGTCAGAAATGACCCG

CAAGAGAAATTGATGTGAGATTGTGATTCGAGTTAACTGTGTGAGAGAGAGACAGGTGACCCCTGTG
CAAGAGAAATTGATGTGAGATTGTGATTCGAGTTAACTGTGTGAGAGAGAGACAGGTGACCCCTGTG

CTGTGAGATGTCGGAAGGTGTGACACAGTACAGAGAGATGGGACACATGTGACATGTGACACAGAGAGAG
CTGTGAGATGTCGGAAGGTGTGACACAGTACAGAGAGATGGGACACATGTGACATGTGACACAGAGAGAG

TGAGAGGACCAACCCCGGCTTCACATACAGTGTGATTCGCAATGTGATGTGACATGTGACATGTGACAGAG
TGAGAGGACCAACCCCGGCTTCACATACAGTGTGATTCGCAATGTGATGTGACATGTGACATGTGACAGAG

TTTCCAGAGACCAATCCGACAGATTGTGCAATTTCTTCTTCCACTTTAACTGTGAAACAGGAGAC
TTTCCAGAGACCAATCCGACAGATTGTGCAATTTCTTCTTCCACTTTAACTGTGAAACAGGAGAC

TTTGTGTGTTCATGTGTGTTCACAAAGAGAGCATGTGTGGGAGTACATGTGTATGTCTTCCAA
TTTGTGTGTTCATGTGTGTTCACAAAGAGAGCATGTGTGGGAGTACATGTGTATGTCTTCCAA

TGACAGCAGCTCAGCTGATGTTCACAAAGAGAGCATGTGTGGGAGTACATGTGTATGTCTTCCAA
TGACAGCAGCTCAGCTGATGTTCACAAAGAGAGCATGTGTGGGAGTACATGTGTATGTCTTCCAA

CGGAAATTTATTTGGGGGGGGTCTGTGTGTGTCTTGTGTGTACTGTGTGACCTGTGATGATGTGGGAGT
CGGAAATTTATTTGGGGGGGGTCTGTGTGTGTCTTGTGTGTACTGTGTGACCTGTGATGATGTGGGAGT

CTGTGTGTGTGTGTGTGTGTGTCTTGT
CTGTGTGTGTGTGTGTGTGTGTCTTGT

GAACCCAGAGAGAAACAGAGATGAGATGTATCTATCCGACATGTGACAGAGAGGAGGAGCTTTCAGAG
GAACCCAGAGAGAAACAGAGATGAGATGTATCTATCCGACATGTGACAGAGAGGAGGAGCTTTCAGAG

ACACAAATGTACATGT
ACACAAATGTACATGT

GT
GT

SBQIND_25
g113448824 |JMB3

AGCTAGACATCTACAGAAAGCTTTTTCGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
g113448824 |JMB3

Submit sequences to:



```
SBQIDNO_25      TCATACAAACCAACATGAAATAGAGAAATTTCTCTCAAGATGACCCGGTAAATATACAC
g113448824|JMK3

SBQIDNO_25      AAGAAACCGAAACTGGGTGCTTCATCTGATGGGTCTTAATCTGTTCGTGCTGATTT
g113448824|JMK3

SBQIDNO_25      CCCCCTGATATTTAGGTGATCTTTAAGAGTTTGCCTACGTAAACCCCGTGTGGGC
g113448824|JMK3

SBQIDNO_25      CTGTGAAACCAACATGTTTCAACACTGTGTGTTCAGACACCAACACACACATGTGAAAT
g113448824|JMK3

SBQIDNO_25      GCGGAGGTGCTGTGACACACACACACACACACACACACACACACACACACACACACAC
g113448824|JMK3

SBQIDNO_25      AACACACACACACCTTAATCTGACACACACACACACACACACACACACACACACACAC
g113448824|JMK3

SBQIDNO_25      CCTGATTCGTGTGTGATGTGTCAATGTGTGAGAGCTTTTGTGATCAGATTTTGTAAAA
g113448824|JMK3

SBQIDNO_25      CAAACCAAAATCAGAGAGTAAATTTGTGTCTGTGAGAGAGATCTTGTCTGAGAGACCTG
g113448824|JMK3

SBQIDNO_25      CTTGTTCACACAGGTGTGAGATTTAAGGAAACCTTCTTAAAGCTAAGTCTGAAATG
g113448824|JMK3

SBQIDNO_25      GTACGAAATATGATCTTTCTATGAGCTGTGTATTTTATTAATTTTACATCTAAATTT
g113448824|JMK3

SBQIDNO_25      TTGCTAAGAGATGATTTTGTGATTTATGAAAAGAAAAATTTCTAATTTAACTGTAAATATAT
g113448824|JMK3

SBQIDNO_25      GTCAATACAAATGTAAATTAACCTATTTTAAAAAAGTTCAACCTTAAGGTAGAGTTCC
g113448824|JMK3

SBQIDNO_25      AAGCTAAGTATGATTAATATGGAATATCAATTAATTAAGTATTTTAACCAAGAAATC
g113448824|JMK3

SBQIDNO_25      TTCTCAGGGAGATTTACTGTGATGTGTCTTTTCCCGC
g113448824|JMK3
```